

WEST Search History

[Hide Items](#)[Restore](#)[Clear](#)[Cancel](#)

DATE: Tuesday, May 29, 2007

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L6	bacteriocin AND cancer	283
<input type="checkbox"/>	L5	(Hetz OR Bono OR Barros OR Lagos)[IN] AND (bacteriocin)	3
<input type="checkbox"/>	L4	(Hetz OR Bono OR Barros OR Lagos)[IN] AND (E492 OR Microcin)	1
<input type="checkbox"/>	L3	(Soto OR Lagos)[IN] AND (bacteriocin)	3
<input type="checkbox"/>	L2	(Soto OR Lagos)[IN] AND (bacteriocin AND apoptosis)	2
<input type="checkbox"/>	L1	bacteriocin AND apoptosis AND cancer	65

END OF SEARCH HISTORY



A service of the National Library of Medicine
and the National Institutes of Health

My NCBI
[Sign In] [Reg]

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Bc

Search PubMed for [] [Preview] [Go] [C]

Limits Preview/Index **History** Clipboard Details

About Entrez

Text Version

Entrez PubMed

Overview

Help | FAQ

Tutorials

New/Noteworthy

E-Utilities

PubMed Services

Journals Database

MeSH Database

Single Citation Matcher

Batch Citation Matcher

Clinical Queries

Special Queries

LinkOut

My NCBI

Related Resources

Order Documents

NLM Mobile

NLM Catalog

NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

- Search History will be lost after eight hours of inactivity.
- Search numbers may not be continuous; all searches are represented.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search	Most Recent Queries	Time	Result
#32	Search Soto and bacteriocin	09:53:28	<u>3</u>
#25	Search Lagos and bacteriocin	09:51:23	<u>22</u>
#29	Related Articles for PubMed (Select 9244266)	09:49:41	<u>198</u>
#24	Search microcin and cancer	09:45:27	<u>1</u>
#23	Search E492 and cancer	09:45:01	<u>1</u>
#22	Search E492 and bacteriocin and cancer	09:44:56	<u>0</u>
#17	Search bacteriocin and cancer	09:16:16	<u>42</u>
#16	Search Muller and Gunther and Naumann	08:29:42	<u>1</u>
#15	Search Muller and Gunther	08:29:32	<u>94</u>
#13	Search Buckley and Brodsky	08:26:11	<u>13</u>
#12	Search Nelson and Buckley	08:26:02	<u>0</u>
#11	Search Nelson and Brodsky	08:25:44	<u>0</u>
#9	Search weinrauch and zychlinsky	08:23:00	<u>7</u>
#8	Search Weinrauch and Zychlinsky	08:22:59	<u>167</u>
#7	Search Leland and Taguchi	08:22:30	<u>1</u>
#1	Search bacteriocin and apoptosis	08:03:29	<u>6</u>

Clear History

Write to the Help Desk

NCBI | NLM | NIH

Department of Health & Human Services

Privacy Statement | Freedom of Information Act | Disclaimer

Apr 30 2007 04:56:27

SCORE Search Results Details for Application 10506857 and Search Result 20070524_133303_us-10-506-857-2.rag.

Score Home Retrieve Application SCORE System SCORE Comments/FAQ Suggestions

This page gives you Search Results detail for the Application 10506857 and Search Result 20070524_133303_us-10-506-857-2.rag.

[Go Back to previous page](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2007, 15:40:52 ; Search time 256 Seconds
(without alignments)
160.563 Million cell updates/sec

Title: US-10-506-857-2
Perfect score: 442
Sequence: 1 GETDPNTQLDLGNNAWG.....SWNGSGYGNATSSSGSGS 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	442	100.0	84	7	ABR83126		AbR83126 K. pneumo
2	442	100.0	103	7	ABR83125		AbR83125 K. coli m
3	172	38.9	74	7	ABR83128		AbR83128 E. coli m
4	172	38.9	74	7	ABR83127		AbR83127 E. coli m
5	101	22.9	1958	2	AAR60620		AAR60620 Protein f
6	97.5	22.1	985	4	ABB57774		Abb57774 Drosophil
7	97.5	22.1	985	8	ADI30147		Adi30147 Drosophil
8	97.5	22.1	985	8	ADI30143		Adi30143 Drosophil
9	97.5	22.1	1019	4	ABB67198		Abb67198 Drosophil
10	97.5	22.1	3190	4	AAB84634		AAB84634 Amino aci
11	90.5	20.5	3275	4	ABB70437		Abb70437 Drosophil
12	90.5	20.5	3275	7	ADK11301		Adk11301 Drosophil
13	88	19.9	242	8	ADV05705		Adv05705 Plant ful
14	87.5	19.8	293	8	ADT60979		Adt60979 Plant pol
15	87.5	19.8	293	8	ADT60977		Adt60977 Plant pol
16	87.5	19.8	529	8	ADX80040		Adx80040 Plant ful
17	85.5	19.3	185	4	AAU32997		AAU32997 Novel hum
18	85	19.2	1953	6	AAE36881		Aae36881 Drosophi
19	84.5	19.1	1465	4	ABB65501		Abb65501 Drosophi
20	84	19.0	162	8	ADG08762		Ado08762 Novel sur
21	84	19.0	162	8	ADG08762		Ado08762 Human-der
22	84	19.0	322	8	ADU08763		Adv78657 Human-der
23	84	19.0	322	9	ADV78657		Adv78657 Cell adhe
24	84	19.0	322	9	AEO05673		Aee05673 Human leu
25	84	19.0	476	8	ADU47941		Adu47941 Human leu
26	84	19.0	476	9	AEC90300		Aec90300 Human leu
27	84	19.0	482	8	ADU08764		Ado08764 Novel sur
28	84	19.0	482	9	ADU78658		Adv78658 Human-der
29	84	19.0	500	8	ADU47940		Adu47940 Human leu
30	84	19.0	500	9	AEC90299		Aec90299 Human leu
31	84	19.0	505	6	ABU34417		Abu34417 Protein e
32	84	19.0	615	6	ABU36862		Abu36862 Protein e
33	84	19.0	615	9	ABU36862		Abu36862 Microbial
34	83.5	18.9	694	9	ABU36802		Abu36802 Protein e
35	83.5	18.9	694	9	ABU36802		Abu36802 Microbial
36	83	18.8	115	3	AAB24825		Aab24825 Plant SDF
37	83	18.8	115	3	AAG29163		Aag29163 Arabidops
38	83	18.8	119	3	AAG25472		Aag25472 Arabidops
39	83	18.8	801	9	ABU36971		Abu36971 Protein e
40	83	18.8	1381	6	ABU36971		Abu36971 Microbial
41	83	18.8	1381	9	ABU36971		Abu36971 Protein e
42	82	18.6	425	4	ABB69033		Abb69033 Drosophil
43	82	18.6	731	6	ABJ19398		Abj19398 Human int
44	82	18.6	876	10	AEI57435		Aei57435 Thale cre
45	82	18.6	2430	10	AEI55629		Aei55629 Thale cre

ALIGNMENTS

RESULT 1
ABR83126
ID ABR83126 standard; protein: 84 AA.
XX
AC ABR83126;

XX 15-JAN-2004 (first entry)
DT
XX
DE K. pneumoniae microcin E492 processed sequence.
XX
XX Microcin E492; apoptosis; bacteriocin; cytostatic; antibacterial;
KW antipsoriatic; gene therapy; gram-negative bacterium.
XX
XX Klebsiella pneumoniae.
OS
XX
XX W02003074554-A2.
PN
XX
XX 12-SEP-2003.
PD
XX
XX 05-MAR-2003; 2003WO-1B000821.
PF
XX
XX 05-MAR-2002; 2002US-0361804P.
PR
XX
XX (GALI-) FUNDACION GALILEO.
PA
XX
XX Soto C, Lagos R;
PI
XX
XX WPI; 2003-748269/70.
DR
XX
XX New bacterial apoptotic-bacteriocin useful for killing bacterial cells or
PT for treating or preventing cancer, tumors and other diseases of aberrant
PT cell growth (e.g. psoriasis or polyps) without being cytotoxic to normal
PT cells.
XX
XX
PS Claim 5; Fig 7; 73pp; English.
XX
XX The invention relates to an isolated bacterial apoptotic-bacteriocin, or
CC its derivative, capable of inducing apoptosis in eukaryotic tumour cells,
CC cancer cells or cells undergoing aberrant growth, where the apoptotic-
CC bacteriocin is not toxic to normal eukaryotic cells. The composition and
CC methods are useful for killing bacterial cells or for treating or
CC preventing cancer, tumors and other diseases of aberrant cell growth
CC (e.g. psoriasis or polyps). The present sequence represents an active and
CC processed sequence of microsin E492 protein, a specific example of an
CC apoptogenic bactericin protein. Microsin E492 is a low-molecular weight
CC channel-forming bacteriocin produced by gram-negative bacterium K.
CC pneumoniae RYC492
XX
SQ Sequence 84 AA:
Query Match 100.0%; Score 442; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.8e-37;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GETDPNTOLLNDLGNNAWGAALCAPGGLGSAALGAAGALQTVCGGLDHGPNVPIPV 60
Db 1 GETDPNTOLLNDLGNNAWGAALCAPGGLGSAALGAAGALQTVCGGLDHGPNVPIPV 60
QY 61 LIGPSWNGSGSGYNSATSSSGSGS 84
Db 61 LIGPSWNGSGSGYNSATSSSGSGS 84
RESULT 2
ABR83125
ID ABR83125 standard; protein; 103 AA.

XX ABR83125;
AC
XX 15-JAN-2004 (first entry)
DT
XX
DE K. pneumoniae microcin E492 unprocessed sequence.
XX
XX Microcin E492; apoptosis; bacteriocin; cytostatic; antibacterial;
KW antipsoriatic; gene therapy; gram-negative bacterium.
XX
XX Klebsiella pneumoniae.
OS
XX
XX W02003074554-A2.
PN
XX
XX 12-SEP-2003.
PD
XX
XX 05-MAR-2003; 2003WO-1B000821.
PF
XX
XX 05-MAR-2002; 2002US-0361804P.
PR
XX
XX (GALI-) FUNDACION GALILEO.
PA
XX
XX Soto C, Lagos R;
PI
XX
XX WPI; 2003-748269/70.
DR
XX
XX New bacterial apoptotic-bacteriocin useful for killing bacterial cells or
PT for treating or preventing cancer, tumors and other diseases of aberrant
PT cell growth (e.g. psoriasis or polyps) without being cytotoxic to normal
PT cells.
XX
XX
PS Claim 5; Fig 6; 73pp; English.
XX
XX The invention relates to an isolated bacterial apoptotic-bacteriocin, or
CC its derivative, capable of inducing apoptosis in eukaryotic tumour cells,
CC cancer cells or cells undergoing aberrant growth, where the apoptotic-
CC bacteriocin is not toxic to normal eukaryotic cells. The composition and
CC methods are useful for killing bacterial cells or for treating or
CC preventing cancer, tumors and other diseases of aberrant cell growth
CC (e.g. psoriasis or polyps). The present sequence represents an
CC unprocessed sequence of microsin E492 protein, a specific example of an
CC apoptogenic bactericin protein. Microsin E492 is a low-molecular weight
CC channel-forming bacteriocin produced by gram-negative bacterium K.
CC pneumoniae RYC492
XX
SQ Sequence 103 AA:
Query Match 100.0%; Score 442; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.5e-37;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GETDPNTOLLNDLGNNAWGAALCAPGGLGSAALGAAGALQTVCGGLDHGPNVPIPV 60
Db 20 GETDPNTOLLNDLGNNAWGAALCAPGGLGSAALGAAGALQTVCGGLDHGPNVPIPV 79
QY 61 LIGPSWNGSGSGYNSATSSSGSGS 84
Db 80 LIGPSWNGSGSGYNSATSSSGSGS 103
RESULT 3

SCORE Search Results Details for Application 10506857 and Search Result 20070524_133305_us-10-506-857-2.rup.

Score Home Retrieve Application SCORE System SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10506857 and Search Result 20070524_133305_us-10-506-857-2.rup.

[Go Back to previous page](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2007, 15:45:18 ; Search time 354 Seconds
(without alignments)
254.402 Million cell updates/sec

Title: US-10-506-857-2
Perfect score: 442
Sequence: 1 GETPNTOLLGNMANG.....SWNGSGGNSATSSSGSGS 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues
Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	100.0	103	1 MCEA_KLEPN	0924n4 klebsiella
2	172	38.9	90	1 MTFS_ECOLI	Q46971 escherichia
3	103	23.3	1733	1 VNVA_PRVKA	P33485 pseudorabie

4	103	23.3	1733	2	Q5PPC8_9ALPH	Q5ppc8 suid herpes
5	101	22.9	1958	2	Q69340_9ALPH	Q69340 suid herpes
6	97.5	22.1	748	2	Q95TP4_DROME	Q95tp4 drosophila
7	97.5	22.1	985	1	KCNAB_DROME	P17970 drosophila
8	97.5	22.1	3190	2	O01368_DROME	O01368 drosophila
9	97.5	22.1	3276	2	Q9W321_DROME	Q9w321 drosophila
10	94.5	21.4	393	2	Q18880_CAEEL	Q18880 caenorhabdi
11	93.5	21.2	227	2	Q628R3_ORYSA	Q628r3 oryza sativ
12	93.5	21.2	987	2	Q37161_RHOPA	Q37161 rhodopseudo
13	93	21.0	838	2	Q4P459_USTWA	Q4p459 ustilago ma
14	93	21.0	1198	2	Q206M1_9ARAC	Q206m1 latrodectus
15	91	20.6	275	2	Q4C9F5_CROWT	Q4c9f5 crocospaer
16	91	20.6	542	2	Q4G1Y1_9ARAC	Q4g1y1 latrodectus
17	91	20.6	769	2	Q4PAD8_USTWA	Q4pad8 ustilago ma
18	90.5	20.5	1352	2	Q2VZW5_MAGWM	Q2vzw5 magnetospir
19	89	20.1	324	2	Q4JT02_CORJK	Q4jt02 corynebacte
20	89	20.1	388	2	Q61FQ1_CAEER	Q61fq1 caenorhabdi
21	89	20.1	536	2	Q3R5X8_XYLEA	Q3r5x8 xylella fas
22	89	20.1	536	2	Q3RGG7_XYLEA	Q3rgg7 xylella fas
23	89	20.1	1849	2	Q2L295_BORAL	Q2l295 bordetella
24	88.5	20.0	226	2	Q4P729_USTWA	Q4p729 ustilago ma
25	88.5	20.0	331	2	Q4DLB6_TRYCR	Q4dlb8 trypanosoma
26	88	19.9	594	2	Q3R7F1_XYLEA	Q3r7f1 xylella fas
27	88	19.9	749	2	Q7TWK6_MYCBO	Q7twk6 mycobacteri
28	87.5	19.8	145	2	Q5GOV3_PINTA	Q5gov3 pinus taeda
29	87.5	19.8	260	2	Q5YU91_NOCEA	Q5yu91 nocardia fa
30	87.5	19.8	315	2	Q1WM90_PINFU	Q1mw90 pinctada fu
31	87.5	19.8	868	2	Q7U2D8_MYCBO	Q7u2d8 mycobacteri
32	87.5	19.8	1578	2	Q2KG58_MAGBR	Q2kg58 magnaporthe
33	87	19.7	770	2	Q354P5_9BRAD	Q354p5 bradyrhizob
34	86.5	19.6	187	2	Q8XVR5_RALSO	Q8xvr5 ralstonia s
35	86.5	19.6	814	2	Q7Q114_ANOGA	Q7q114 anopheles g
36	86.5	19.6	1435	2	Q4LJR7_9BURK	Q4ljr7 burkholderi
37	86.5	19.6	1435	2	Q1BG64_9BURK	Q1bg64 burkholderi
38	86	19.5	348	2	Q4MLV4_ASPEU	Q4mlv4 aspergillus
39	86	19.5	583	2	Q7PMR9_ANOGA	Q7pmr9 anopheles g
40	86	19.5	831	2	Q7U159_MYCBO	Q7u159 mycobacteri
41	86	19.5	879	2	Q8VKD2_MYCTU	Q8vkd2 mycobacteri
42	86	19.5	882	2	Q79FV6_MYCTU	Q79fv6 mycobacteri
43	86	19.5	1360	2	Q7TWC4_MYCBO	Q7twc4 mycobacteri
44	86	19.5	1579	2	Q7KOM6_DROME	Q7kqm6 drosophila
45	86	19.5	2615	2	Q2GGU5_NOVAD	Q2ggu5 novosphingo

ALIGNMENTS

RESULT 1
MCEA_KLEPN
ID _MCEA_KLEPN STANDARD; PRT; 103 AA.
AC Q924N4; 982562;
DT 04-MAY-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Microcin E492 precursor (MccE492).
GN Name=mceA;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN (1)

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], PARTIAL PROTEIN SEQUENCE, AND
RP CHARACTERIZATION.
RX STRAIN=RYC492;
RX MEDLINE=99084959; PubMed=9864332;
RA Lagos R., Villanueva J.E., Monasterio O.;
RT "Identification and properties of the genes encoding microcin E492 and
RT its immunity protein.";
RL J. Bacteriol. 181:212-217(1999).
RN [2]
RP PROTEIN SEQUENCE OF 20-103, AND MASS SPECTROMETRY.
RA Pons A.M., Vignon D., Cotteau G.;
RL Submitted (FEB-2001) to Swiss-Prot.
RN [3]
RP PARTIAL PROTEIN SEQUENCE, AMINO-ACID COMPOSITION, SIDEROPHORE BINDING
RP SITE, AND MASS SPECTROMETRY.
RX STRAIN=RYC492;
RX PubMed=15102848; DOI=10.1074/jbc.M400228200;
RA Thomas X., Destoumieux-Garzon D., Peduzzi J., Afonso C., Blond A.,
RA Bitlirakis N., Goulard C., Dubost L., Thal R., Tabet J.-C.,
RA Rebuffat S.;
RT "Siderophore peptide, a new type of post-translationally modified
RT antibacterial peptide with potent activity.";
RL J. Biol. Chem. 279:28233-28242(2004).
RN [4]
RP CHARACTERIZATION.
RX STRAIN=RYC492;
RX MEDLINE=93238942; PubMed=7682973; DOI=10.1016/0014-5793(93)80096-D;
RA Lagos R., Wilkens M., Vergara C., Cecchi X., Monasterio O.;
RT "Microcin E492 forms ion channels in phospholipid bilayer membrane.";
RL FEBS Lett. 321:145-148(1993).
CC -!- FUNCTION: Channel-forming bacteriocin. Forms cation-selective
CC channels. Active on enterobacteria.
CC -!- PTM: The C-terminal Ser is modified by attachment to a siderophore
CC similar to enterobactin, which can bind one atom of iron. The
CC modification consists of an ester linkage of the serine carboxyl
CC to O6 of a glucose which is linked by a C-glycosidic bond to the
CC 5'-benzoyl of a linear triester of N-(2,3-dihydroxybenzoyl)serine.
CC -!- MASS SPECTROMETRY: MW=7886.68; MW_ERR=0.52; METHOD=Electrospray;
CC RANGE=20-103; NOTE=Ref.2.
CC -!- MASS SPECTROMETRY: MW=7887; METHOD=MALDI; RANGE=20-103; NOTE=Ser-
CC 103 unmodified form (Ref.3).
CC -!- MASS SPECTROMETRY: MW=8718; METHOD=MALDI; RANGE=20-103; NOTE=Ser-
CC 103 modified form (Ref.3).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF063590; AAD04332.1; -; Genomic DNA.
KW Antibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;
FT SIGNAL
FT CHAIN 1 19 Microcin E492.
FT CHAIN 20 103 /FTId=PRO_0000005677.
FT MOD_RES 103 103 Serine microcin E492 siderophore ester.
FT SEQUENCE 103 AA; 10091 MW; 8AC1376E89F9E421 CRC64;
SQ
Query Match 100.0%; Score 442; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.5e-32;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GETDPNTQLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIPV 60

Db 20 GETDPNTQLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIPV 79
Qy 61 LIGPSWNGSGSYNSATSSSGSGS 84
Db 80 LIGPSWNGSGSYNSATSSSGSGS 103
RESULT 2
MTFS_ECOLI
ID MTFS_ECOLI STANDARD; PRT; 90 AA.
AC Q46971;
DT 04-MAY-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Microcin-24 precursor (Mcc24).
GN Name=mtfs;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=2424;
RA O'Brien G.J., Mahanty H.K.;
RT "Complete nucleotide sequence of microcin 24 genetic region and
RT analysis of a new ABC transporter.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Channel-forming bacteriocin (By similarity).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL: U47048; AA88772.1; -; Genomic DNA.
KW Antibiotic; Antimicrobial; Bacteriocin; Signal.
FT SIGNAL 1 16 By similarity.
FT CHAIN 17 90 Microcin-24.
FT SEQUENCE 90 AA; 9425 MW; 2EA068A7048D8169 CRC64;
SQ
Query Match 38.9%; Score 172; DB 1; Length 90;
Best Local Similarity 55.2%; Pred. No. 8.4e-08;
Matches 37; Conservative 7; Mismatches 21; Indels 2; Gaps 2;
Qy 4 DPNQTLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIPV 62
Db 23 DPNQTLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIPV 81
Qy 63 GPSWNGS 69
Db 82 GPSWNGS 88
RESULT 3
VNUA_PRVKA
ID VNUA_PRVKA STANDARD; PRT; 1733 AA.
AC P33485;
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1994, sequence version 1.
DT 30-MAY-2006, entry version 16.
DE Probable nuclear antigen.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10506857 and Search Result 20070524_1...

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: May 24, 2007, 15:49:50 ; Search time 39 Seconds
(without alignments)
207.236 Million cell updates/sec

Title: US-10-506-857-2
Perfect score: 442
Sequence: 1 GETDPNTQLNDLGNNAWG.....SWNGSGSYNSATSSSGSGS 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80**
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	103	23.3		1733	1	B45344	probable nuclear a
2	101	22.9		1958	2	B40505	hypothetical prote
3	97.5	22.1		924	2	B41359	potassium channel
4	97.5	22.1		924	2	S12746	potassium channel
5	97.5	22.1		3190	2	T13828	CREB-binding prote
6	96.5	21.8		575	2	S53327	protein kinase egg
7	94.5	21.4		393	2	T20268	hypothetical prote

8	86	19.5	882	2	B70812	hypothetical glyci
9	84.5	19.1	205	2	T07959	probable cell wall
10	84	19.0	615	2	T07959	hypothetical glyci
11	83.5	18.9	694	2	T08868	hypothetical glyci
12	83	18.8	115	2	T08958	glycine-rich prote
13	83	18.8	801	2	T08824	hypothetical glyci
14	83	18.8	839	2	T75518	hypothetical prote
15	83	18.8	1381	2	T08006	hypothetical glyci
16	82.5	18.7	970	2	T07533	probable sulfatase
17	81.5	18.4	464	2	E82865	conjugal transfer
18	81.5	18.4	498	2	T07020	hypothetical glyci
19	81	18.3	384	1	A26099	glycine-rich cell
20	80.5	18.2	459	2	F83602	hypothetical prote
21	80.5	18.2	731	2	T07974	hypothetical glyci
22	80.5	18.2	2329	2	T28125	hypothetical prote
23	80	18.1	331	2	T08020	hypothetical glyci
24	79.5	18.0	591	2	B70523	hypothetical glyci
25	79.5	18.0	914	2	H70987	hypothetical glyci
26	79.5	18.0	3157	2	B70969	probable PPE prote
27	79	17.9	198	2	A10632	tip repressor bind
28	78.5	17.8	347	2	B39112	marzoite 45K surf
29	78.5	17.8	396	2	T49109	glycine-rich prote
30	78.5	17.8	586	2	T26667	hypothetical prote
31	78.5	17.8	603	2	A70770	hypothetical glyci
32	78.5	17.8	778	2	F70963	hypothetical glyci
33	78.5	17.8	1097	2	T13033	cyclin T - fruit f
34	78.5	17.8	1329	2	E70917	hypothetical glyci
35	78	17.6	290	2	T23416	hypothetical prote
36	78	17.6	1341	2	H98323	hypothetical prote
37	77.5	17.5	183	1	KNRZG2	glycine-rich cell
38	77.5	17.5	194	2	S24297	chorion protein -
39	77.5	17.5	252	1	S01821	glycine-rich prote
40	77.5	17.5	383	2	C87478	hypothetical prote
41	77.5	17.5	434	2	E70768	hypothetical glyci
42	77.5	17.5	532	2	F70580	hypothetical glyci
43	77.5	17.5	783	2	E70824	hypothetical glyci
44	77	17.4	812	2	S31521	collagen COLF1 - f
45	77	17.4	837	2	E70835	hypothetical glyci

ALIGNMENTS

RESULT 1
B45344

probable nuclear antigen - suid herpesvirus 1 (strain Kaplan)
C:Species: suid herpesvirus 1
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: B45344
R:VLcek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzler, M.
Virology 179, 365-377, 1990
A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented
A:Reference number: A45344; MUID:91021039; PMID:2171211
A:Accession: B45344

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1733 <VLCC>
A:Cross-references: UNIPROT:P33485; UNIPARC:UPI0000138ADE; GB:M34651; NID:g334070; PIC
C:Superfamily: pseudorabies virus 1 nuclear antigen
Query Match 23.3% Score 103; DB 1; Length 1733;

[illegible]

```

Query Match      22.1%; Score 97.5; DB 2; Length 924;
Best Local Similarity 34.0%; Pred. No. 0.33;
Matches 32; Conservative 12; Mismatches 25; Indels 25; Gaps 5;

Qy    12 DLGNNNWAGAAALGAP-----GGIGSALMGAGGALQTVG-----QGII-----DHGPVNVP I 58
      |   | :| :|| ||:| :| ||||| :| ||| :| :|
Db    84 DTSNGNWDWRAMGAGAGAYGGIIGSLPAGGAAYHLGPANPAGILVSRHLDYGDGG--- 140
      |   | | | | | | | | | | :| :| | | | |
Qy    59 PVLIGPS-----WNKSGSYNSATSSSGSGS 84
      |   | | | | | | | | | | :| :| | | | |
Db    141 -HLAIPAGLPGAVGSGAGAGASVTGSGS 173

RESULT 4
SI2746
potassium channel protein shabll - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: SI2746; S15058
R:Butler, A.; Wei, A.; Salkoff, L.
Nucleic Acids Res. 18, 2173-2174, 1990
A:Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila.
A:Reference number: SI2746; MUID:90245668; PMID:2136395
A:Accession: SI2746
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
A:Cross-references: UNIPROT:P17970; UNIPARC:UPI0000177956; EMBL:M32659
R:Butler, A.; Wei, A.; Salkoff, L.
submitted to the EMBL Data Library, March 1990
A:Description: Shal, Shab, and Shaw: Three genes encoding potassium channels in Drosop
A:Reference number: S15058
A:Accession: SI2746
A:Molecule type: mRNA
A:Residues: 1-625.'YG'.628-924 <BU2>
A:Cross-references: UNIPARC:UPI0000168D76; EMBL:M32659; NID:g158458; PIDN:AAA28896.1;
C:Genetics:
A:Gene: shabll
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drkl
C:Keywords: ion channel; potassium channel; transmembrane protein

Query Match      22.1%; Score 97.5; DB 2; Length 924;
Best Local Similarity 34.0%; Pred. No. 0.33;
Matches 32; Conservative 12; Mismatches 25; Indels 25; Gaps 5;

Qy    12 DLGNNNWAGAAALGAP-----GGIGSALMGAGGALQTVG-----QGII-----DHGPVNVP I 58
      |   | :| :|| ||:| :| ||||| :| ||| :| :|
Db    84 DTSNGNWDWRAMGAGAGAYGGIIGSLPAGGAAYHLGPANPAGILVSRHLDYGDGG--- 140
      |   | | | | | | | | | | :| :| | | | |
Qy    59 PVLIGPS-----WNKSGSYNSATSSSGSGS 84
      |   | | | | | | | | | | :| :| | | | |
Db    141 -HLAIPAGLPGAVGSGAGAGASVTGSGS 173

RESULT 5
TI13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: TI13828

```


SCORE Search Results Details for Application 10506857 and Search Result 20070524_133312 10-506-857-2.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10506857 and Search Result 20070524_133312_us-10-506-857-2.ra.

Go Back to pr

GenCore version 6.2.1

Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2007, 15:51:20 ; Search time 63 Seconds (without alignments) 116.708 Million Cell updates/sec

Title: US-10-506-857-2

Perfect score: 442 Sequence: 1 GETDPTQLNDLGNMANG.....SWNGSGSYNSATSSGSGS 84

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents AA:* 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
------------	-------------	--------------	----	-------------

1	101	22.9	1958	1	US-07-945-283-2	Sequence 2, Appli
2	86	19.5	376	2	US-09-270-167-43474	Sequence 43474, A
3	85	19.2	541	2	US-09-248-796A-26119	Sequence 26119, A
4	81	18.3	428	2	US-09-248-796A-20582	Sequence 20582, A
5	80.5	18.2	539	2	US-09-252-991A-31813	Sequence 31813, A
6	80.5	18.2	2870	2	US-09-479-467A-15	Sequence 15, Appli
7	80.5	18.2	2870	2	US-09-655-160-15	Sequence 15, Appli
8	80.5	18.2	3178	2	US-09-473-467A-4	Sequence 4, Appli
9	80.5	18.2	3178	2	US-09-655-160-4	Sequence 4, Appli
10	80	18.1	262	1	US-08-397-633A-73	Sequence 73, Appli
11	79.5	18.0	486	1	US-08-397-633A-77	Sequence 77, Appli
12	78.5	17.8	123	1	US-07-609-716-103	Sequence 103, App
13	78.5	17.8	123	2	US-08-475-411A-103	Sequence 103, App
14	78.5	17.8	123	2	US-08-478-029A-103	Sequence 103, App
15	78.5	17.8	159	1	US-07-609-716-104	Sequence 104, App
16	78.5	17.8	159	2	US-08-475-411A-104	Sequence 104, App
17	78.5	17.8	159	2	US-08-478-029A-104	Sequence 104, App
18	78.5	17.8	333	1	US-08-712-948-1	Sequence 1, Appli
19	78.5	17.8	832	1	US-08-209-747-2	Sequence 2, Appli
20	78.5	17.8	832	1	US-08-458-288-2	Sequence 2, Appli
21	78.5	17.8	1097	3	US-08-951-188A-4	Sequence 4, Appli
22	77.5	17.5	479	1	US-08-397-633A-78	Sequence 78, Appli
23	77	17.4	239	2	US-09-252-991A-25790	Sequence 25790, A
24	77	17.4	318	2	US-09-060-756-727	Sequence 727, App
25	77	17.4	318	2	US-09-670-314-727	Sequence 727, App
26	77	17.4	318	2	US-10-259-678-727	Sequence 727, App
27	77	17.4	334	2	US-09-060-756-728	Sequence 728, App
28	77	17.4	334	2	US-09-670-314-728	Sequence 728, App
29	77	17.4	334	2	US-10-259-678-728	Sequence 728, App
30	76.5	17.3	437	2	US-09-921-099A-17	Sequence 17, Appli
31	75.5	17.1	528	2	US-09-490-291-8	Sequence 8, Appli
32	75.5	17.1	885	2	US-09-949-016-7789	Sequence 7789, Ap
33	75	17.0	316	2	US-09-538-092-997	Sequence 997, App
34	75	17.0	651	2	US-09-556-978B-19	Sequence 19, Appli
35	75	17.0	651	2	US-09-247-806-1	Sequence 1, Appli
36	75	17.0	651	2	US-09-863-859-1	Sequence 1, Appli
37	75	17.0	651	2	US-09-861-597-1	Sequence 1, Appli
38	75	17.0	651	2	US-10-414-760-1	Sequence 2, Appli
39	75	17.0	718	1	US-08-425-069-2	Sequence 2, Appli
40	75	17.0	718	1	US-08-317-844B-2	Sequence 3, Appli
41	75	17.0	747	2	US-09-034-177-3	Sequence 3, Appli
42	75	17.0	975	2	US-09-328-352-4764	Sequence 4764, Ap
43	74.5	16.9	112	2	US-09-252-991A-31960	Sequence 31960, A
44	74.5	16.9	168	2	US-09-512-342-20	Sequence 20, Appli
45	74.5	16.9	591	2	US-09-134-000C-6729	Sequence 6729, Ap

ALIGNMENTS

RESULT 1
US-07-945-283-2
; Sequence 2, Application US/07945283
; Patent No. 5352596
; GENERAL INFORMATION:
; APPLICANT: Cheung, Andrew K.
; APPLICANT: Wesley, Ronald D.
; TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
; TITLE OF INVENTION: Involving The EPO and LIT Genes
; NUMBER OF SEQUENCES: 7

```

CORRESPONDENCE ADDRESS:
ADDRESS: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
STATE: IL
COUNTRY: USA
ZIP: 61604

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/07/945,283
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
TELEFAX: 309-685-4128
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1958 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-945-283-2

```

Query Match	22.9%	Score 101;	DB 1;	Length 1958;
Best Local Similarity	38.0%;	Pred. No. 0.14;		
Matches	27;	Conservative	8;	Mismatches 28; Indels 8; Gaps 3;
Qy	20	GAALGAPG-GUGSNAALGAAG--GALQTVGQGLIDHGFPNNVIPVLGPSWNGS-----CS 71		
		:		
Db	1050	GRAVGEGGGGPRRVGLAGRAAAVAGRGVLGHGPERAPEPVVLGGGGGGGGGHERGS 1109		
Qy	72	GYNATSSSGS 82		
Db	1110	GVRSGPSEGA 1120		

```

RESULT 2
US-09-270-767-43474
; Sequence 43474, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43474
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43474

```

	Query March	19.58;	Score 96;	DB 2;	Length 376;	
	Best Local Similarity	30.88;	Pred: No. 0.71;	Mismatches 27;	Indels 36;	Gaps 7;
	Matches 33;	Conservative	11;			
Qy	2 ETDPTOLLNDLGNW--AWGAALGAFGGSLGSAAAGACGALTQTVGGLDIDGPV---NV 56					
Dd	127 EEDINGNQ-----NSLGNNRPAAW---LQRSFSGSASGSGRG-----GTVDGRMRGKSA 174					
Qy	57 PIPVLIGPS-----W-----NGSGSYNATSSGSGSGS 84					
Dd	175 YHPIYORPSGLYDELSLVISKAERTWSDRNGTGDSAATTITSGSCA 221					

RESULT 3

```

US-09-248-796A-26119
; Sequence 26119, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26119
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26119

```

```

Query Match      19.2%; Score 85; DB 2; Length 541;
Best Local Similarity 29.2%; Pred. No. 1.3,
Matches 31; Conservative 11; Mismatches 36; Indels 28; Gaps 4;

Qy 1 GETDPNTQLLDGNMNAWGAALGAPGGL-----GSAALGANGA-----LQTV 44
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 GCVPTGGSSGGTGSWMGSGAGSGGTTTSGSGSSSSGASGGTGWGSGNDYVCPG 386
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 45 GQGLDHPGVNVPVLPVLGFSWNWGSQGYNSATSS-----SQSGS 84
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 387 AECYDDEEPDNG-----GSMWGGSGSGSGSGSGSGVSGDSCGS 426
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 4

US-09-248-796A-20582
 ; Sequence 20582, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13

SCORE Search Results Details for Application 10506857 and Search Result 20070524_133315_us-10-506-857-2.rapbm.

[Score Home](#) [Retrieve Application List](#) [SCORE Overview](#) [FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10506857 and Search Result 20070524_133315_us-10-506-857-2.rapbm.

[Go Back to previous](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: May 24, 2007, 15:52:30 ; Search time 421 Seconds
(without alignments)
92.423 Million cell updates/sec

Title: US-10-506-857-2
Perfect score: 442
Sequence: 1 GETDPNTQLNDLGNNAWG.....SWNGSGSYNSATSSGSGS 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

1	442	100.0	84	5	US-10-506-857-2	Sequence 2, Appli
2	442	100.0	103	5	US-10-506-857-1	Sequence 1, Appli
3	172	38.9	74	5	US-10-506-857-4	Sequence 4, Appli
4	172	38.9	90	5	US-10-506-857-3	Sequence 3, Appli
5	97.5	22.1	985	4	US-10-154-086-20	Sequence 20, Appl
6	97.5	22.1	985	6	US-11-097-143-114	Sequence 114, App
7	97.5	22.1	1019	6	US-11-097-143-28386	Sequence 28386, A
8	97.5	22.1	3190	5	US-10-732-923-18448	Sequence 18448, A
9	97.5	22.1	3276	5	US-10-732-923-18447	Sequence 18447, A
10	90.5	20.5	3275	5	US-10-840-060-90	Sequence 90, Appl
11	90.5	20.5	3275	6	US-11-097-143-38103	Sequence 38103, A
12	88.5	20.0	264	4	US-10-437-963-135092	Sequence 135092,
13	88	19.9	242	4	US-10-425-114-61520	Sequence 61520, A
14	88	19.9	594	6	US-11-087-099-1758	Sequence 1758, Ap
15	87.5	19.8	293	5	US-10-739-930-11056	Sequence 11056, A
16	87.5	19.8	295	5	US-10-739-930-11054	Sequence 11054, A
17	87.5	19.8	449	4	US-10-424-599-285485	Sequence 285485,
18	87.5	19.8	529	4	US-10-425-114-49406	Sequence 49406, A
19	86.5	19.6	251	4	US-10-767-701-32417	Sequence 32417, A
20	85.5	19.3	420	4	US-10-437-963-201378	Sequence 201378,
21	85	19.2	1953	5	US-10-488-056-42	Sequence 42, Appl
22	84.5	19.1	1465	6	US-11-097-143-23295	Sequence 23295, A
23	84.5	19.1	1827	4	US-10-437-963-155343	Sequence 155343,
24	84	19.0	476	6	US-11-109-435-16	Sequence 16, Appl
25	84	19.0	500	6	US-11-109-435-15	Sequence 15, Appl
26	84	19.0	503	4	US-10-282-122A-62341	Sequence 62341, A
27	84	19.0	615	4	US-10-282-122A-64786	Sequence 64786, A
28	84	19.0	615	6	US-11-052-554A-152	Sequence 152, App
29	83.5	18.9	152	4	US-10-424-599-202771	Sequence 202771,
30	83.5	18.9	694	4	US-10-282-122A-64726	Sequence 64726, A
31	83.5	18.9	694	6	US-11-052-554A-158	Sequence 158, App
32	83	18.8	80	4	US-10-424-599-241896	Sequence 241896,
33	83	18.8	614	6	US-11-087-099-3677	Sequence 3677, Ap
34	83	18.8	731	5	US-10-732-923-13866	Sequence 13866, A
35	83	18.8	801	6	US-11-052-554A-166	Sequence 166, App
36	83	18.8	1381	4	US-10-282-122A-64895	Sequence 64895, A
37	83	18.8	1381	6	US-11-052-554A-138	Sequence 138, App
38	82.5	18.7	201	4	US-10-425-115-309662	Sequence 309662,
39	82.5	18.7	454	4	US-10-767-701-45105	Sequence 45105, A
40	82.5	18.7	1422	4	US-10-156-761-12633	Sequence 12633, A
41	82	18.6	425	6	US-11-097-143-33891	Sequence 33891, A
42	81.5	18.4	130	4	US-10-424-599-193985	Sequence 193985,
43	81.5	18.4	360	5	US-10-488-056-31	Sequence 31, Appl
44	81.5	18.4	384	4	US-10-479-638-19	Sequence 19, Appl
45	81.5	18.4	498	4	US-10-225-8388-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-506-857-2
; Sequence 2, Application US/10506857
; Publication No. US20050159349A1
; GENERAL INFORMATION:
; APPLICANT: Soto, Claudio
; APPLICANT: Lagos, Rosalba
; TITLE OF INVENTION: APOPTOGENIC-BACTERIOICINS COMBINING BROAD SPECTRUM ANTIBIOTIC AN
; TITLE OF INVENTION: SELECTIVE ANTI-TUMORAL ACTIVITIES, AND COMPOSITIONS AND USES T
; FILE REFERENCE: 2641-1-001PCT

```
; CURRENT APPLICATION NUMBER: US/10/506,857
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/361,804
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-506-857-2

Query Match          100.0%; Score 442; DB 5; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.1e-36;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GETDPNTOLLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIV 60
Db 1 GETDPNTOLLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIV 60

Qy 61 LIGPSWNGSGSYNSATSSSGSGS 84
Db 61 LIGPSWNGSGSYNSATSSSGSGS 84

RESULT 2
US-10-506-857-1
; Sequence 1, Application US/10506857
; Publication No. US20050159349A1
; GENERAL INFORMATION:
; APPLICANT: Soto, Claudio
; APPLICANT: Lagos, Rosalba
; TITLE OF INVENTION: APOPTOGENIC-BACTERIOCINS COMBINING BROAD SPECTRUM ANTIBIOTIC AN
; TITLE OF INVENTION: SELECTIVE ANTI-TUMORAL ACTIVITIES, AND COMPOSITIONS AND USES T
; FILE REFERENCE: 2641-1-001PCT
; CURRENT APPLICATION NUMBER: US/10/506,857
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/361,804
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-506-857-1

Query Match          100.0%; Score 442; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.1e-36;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GETDPNTOLLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIV 60
Db 20 GETDPNTOLLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIV 79

Qy 61 LIGPSWNGSGSYNSATSSSGSGS 84
Db 80 LIGPSWNGSGSYNSATSSSGSGS 103

RESULT 3
```

```
US-10-506-857-4
; Sequence 4, Application US/10506857
; Publication No. US20050159349A1
; GENERAL INFORMATION:
; APPLICANT: Soto, Claudio
; APPLICANT: Lagos, Rosalba
; TITLE OF INVENTION: APOPTOGENIC-BACTERIOCINS COMBINING BROAD SPECTRUM ANTIBIOTIC AN
; TITLE OF INVENTION: SELECTIVE ANTI-TUMORAL ACTIVITIES, AND COMPOSITIONS AND USES T
; FILE REFERENCE: 2641-1-001PCT
; CURRENT APPLICATION NUMBER: US/10/506,857
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/361,804
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-506-857-4

Query Match          38.9%; Score 172; DB 5; Length 74;
Best Local Similarity 55.2%; Pred. No. 1.8e-09;
Matches 37; Conservative 7; Mismatches 21; Indels 2; Gaps 2;

Qy 4 DPNTOLLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIV-VLI 62
Db 7 DNTSQIVRQIMSNAAWGPPL-VPERFRGNMVAAGGVTQTVLQGAHAHPVNPVPIKPEVM 65

Qy 63 GPSWNGS 69
Db 66 GPSWNGS 72

RESULT 4
US-10-506-857-3
; Sequence 3, Application US/10506857
; Publication No. US20050159349A1
; GENERAL INFORMATION:
; APPLICANT: Soto, Claudio
; APPLICANT: Lagos, Rosalba
; TITLE OF INVENTION: APOPTOGENIC-BACTERIOCINS COMBINING BROAD SPECTRUM ANTIBIOTIC AN
; TITLE OF INVENTION: SELECTIVE ANTI-TUMORAL ACTIVITIES, AND COMPOSITIONS AND USES T
; FILE REFERENCE: 2641-1-001PCT
; CURRENT APPLICATION NUMBER: US/10/506,857
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/361,804
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-506-857-3

Query Match          38.9%; Score 172; DB 5; Length 90;
Best Local Similarity 55.2%; Pred. No. 2.2e-09;
Matches 37; Conservative 7; Mismatches 21; Indels 2; Gaps 2;

Qy 4 DPNTOLLNDLGNNAWGAALGAPGGLGSAALGAGGALQTVGGGLIDHGPVNPVPIV-VLI 62
```

SCORE Search Results Details for Application 10

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10506857 and Search Result 20070524

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: May 24, 2007, 15:54:15 ; Search time 129 Seconds
(without alignments)
203.037 Million cell updates/sec

Title: US-10-506-857-2
Perfect score: 442
Sequence: 1 GETDPWTQLNDLGNNAWG.....SWNGSGSYNSATSSGSGS 84

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1306224 seqs, 311806505 residues

Total number of hits satisfying chosen parameters: 1306224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_NEW_PUB pep: *
2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US06_NEW_PUB pep: *
3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_NEW_PUB pep: *
4: /EMC_Celerra_SID33/ptodata/2/pubpaa/PCT_NEW_PUB pep: *
5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_NEW_PUB pep: *
6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10_NEW_PUB pep: *
7: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_NEW_PUB pep: *
8: /EMC_Celerra_SID33/ptodata/2/pubpaa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	100.5	22.7	104	7	US-11-486-448-71847 Sequence 71847, A

2	93.5	21.2	227	6	US-10-449-902-41618	Sequence 41618, A
3	93	21.0	838	7	US-11-330-403-15569	Sequence 15569, A
4	88	19.9	242	7	US-11-520-715-61520	Sequence 61520, A
5	88	19.9	594	7	US-11-330-403-6136	Sequence 6136, Ap
6	88	19.9	749	7	US-11-330-403-9435	Sequence 9435, Ap
7	87.5	19.8	295	7	US-11-241-607-54773	Sequence 54773, A
8	87.5	19.8	529	7	US-11-520-715-49406	Sequence 49406, A
9	87.5	19.8	868	7	US-11-330-403-1186	Sequence 1186, Ap
10	86	19.5	144	7	US-11-443-428A-997717	Sequence 997717, A
11	86	19.5	785	7	US-11-330-403-14489	Sequence 14489, A
12	86	19.5	831	7	US-11-330-403-1019	Sequence 1019, Ap
13	86	19.5	879	7	US-11-330-403-15071	Sequence 15071, A
14	86	19.5	882	7	US-11-330-403-7222	Sequence 7222, Ap
15	86	19.5	1360	7	US-11-330-403-10138	Sequence 10138, A
16	85.5	19.3	518	6	US-10-449-902-54389	Sequence 54389, A
17	85	19.2	541	6	US-10-603-113-26119	Sequence 26119, A
18	84.5	19.1	205	7	US-11-330-403-17000	Sequence 17000, A
19	84.5	19.1	312	6	US-10-703-032-124459	Sequence 124459, A
20	84	19.0	615	7	US-11-330-403-5859	Sequence 5859, Ap
21	84	19.0	615	7	US-11-330-403-12394	Sequence 12394, A
22	84	19.0	663	7	US-11-330-403-1845	Sequence 1845, Ap
23	84	19.0	725	7	US-11-330-403-10875	Sequence 10875, A
24	83.5	18.9	694	7	US-11-330-403-18622	Sequence 18622, A
25	83	18.8	614	7	US-11-330-403-7495	Sequence 7495, Ap
26	83	18.8	658	7	US-11-443-428A-815210	Sequence 815210, A
27	83	18.8	711	7	US-11-443-428A-815195	Sequence 815195, A
28	83	18.8	729	7	US-11-443-428A-815209	Sequence 815209, A
29	83	18.8	731	7	US-11-443-428A-815198	Sequence 815198, A
30	83	18.8	749	7	US-11-443-428A-815200	Sequence 815200, A
31	83	18.8	757	7	US-11-443-428A-815199	Sequence 815199, A
32	83	18.8	770	7	US-11-443-428A-815196	Sequence 815196, A
33	83	18.8	770	7	US-11-443-428A-815206	Sequence 815206, A
34	83	18.8	770	7	US-11-443-428A-815207	Sequence 815207, A
35	83	18.8	801	7	US-11-330-403-6548	Sequence 6548, Ap
36	83	18.8	1381	7	US-11-330-403-13081	Sequence 13081, A
37	83	18.8	1384	7	US-11-330-403-2821	Sequence 2821, Ap
38	82.5	18.7	231	7	US-11-056-355B-16346	Sequence 16346, A
39	82.5	18.7	231	7	US-11-241-607-8643	Sequence 8643, Ap
40	82.5	18.7	249	7	US-11-056-355B-16345	Sequence 16345, Ap
41	82.5	18.7	249	7	US-11-241-607-8642	Sequence 8642, Ap
42	82	18.6	731	6	US-10-480-962-8	Sequence 8, Appli
43	82	18.6	876	7	US-11-174-307B-1902	Sequence 1902, Ap
44	82	18.6	2430	7	US-11-174-307B-96	Sequence 96, Appl
45	81.5	18.4	491	7	US-11-330-403-17618	Sequence 17618, A

ALIGNMENTS

RESULT 1

US-11-486-448-71847
; Sequence 71847, Application US/11486448
; Publication No. US20070061916A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/11/486,448

```
; CURRENT FILING DATE: 2006-07-14
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 71847
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(104)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1565_1.pep
; US-11-4486-448-71847

Query Match      22.7%; Score 100.5; DB 7; Length 104;
Best Local Similarity 42.5%; Pred. No. 0.047;
Matches 31; Conservative 6; Mismatches 21; Indels 15; Gaps 3;

Qy 16 NMWGAALGAPGGLGSAALGAGGALQTVGGQLIDHGPVNPVPIVLIQPSWNGSGSGYNS 75
   | :||| | | | : | || | | | | : | : | || | | | | | | | | | | | | |
Db 12 NAGYGAAGRSRGCTPNSNAGAGGDLQSGGGYMGSGYGDV-----NGS-SCYGS 60

Qy 76 AT-----SSSGSGS 84
   || || || || |
Db 61 ATWSDSSQSGSN 73

RESULT 2
US-10-449-902-41618
; Sequence 41618, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41618
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-41618

Query Match      21.2%; Score 93.5; DB 6; Length 227;
Best Local Similarity 32.2%; Pred. No. 0.46;
Matches 28; Conservative 7; Mismatches 23; Indels 29; Gaps 3;

Qy 12 DLGNMWAALGAPGGLG-----SAALGAAGGALQTVGGQLIDHGPVNPVPI 58
   ||| | : | : | || |
Db 30 DLGVNLGGGLGVGGGGGLGVGTGGGLGSGIGVGIGGGGGGGGGSG----- 78

Qy 59 PVLIGPSWNGSGSG-YNSATSSSGSGS 84
```

```
Db 79 -----SGSYSGSGSGSYSGSGSGSGS 101
   |:||||| | : | |||||

RESULT 3
US-11-330-403-15569
; Sequence 15569, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15569
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Ustilago maydis 521
; US-11-330-403-15569

Query Match      21.0%; Score 93; DB 7; Length 838;
Best Local Similarity 35.2%; Pred. No. 1.9;
Matches 25; Conservative 5; Mismatches 23; Indels 18; Gaps 2;

Qy 14 GNNMWAALGAPGGLGSAALGAGGALQTVGGQLIDHGPVNPVPIVLIQPSWNGSGSGY 73
   || || | : | || | | : | : | | | | | | | | | | | | | | | | | | | |
Db 73 GNGAGWGSYSGSGSGSGS---GSGSGSGSGSGSG-----SGSGSGSGSGS 114

Qy 74 NSATSSSGSGS 84
   | | | | |||
Db 115 GSGTKSPSGS 125

RESULT 4
US-11-520-715-61520
; Sequence 61520, Application US/11520715
; Publication No. US20070011783A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/11/520,715
; CURRENT FILING DATE: 2006-09-14
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61520
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-024-A5_FLI.pep
; US-11-520-715-61520

Query Match      19.9%; Score 88; DB 7; Length 242;
Best Local Similarity 32.9%; Pred. No. 1.6;
```